

## SEQUENCE LISTING

<120> BETA-CAP73 CONTROL OF NORMAL AND ABNORMAL CELL MIGRATION

<130> TUI-001CP <140> US 09/750,590 <141> 2000-12-28 <150> 60/170,182 <151> 1999-12-10 <150> 09/733,818 <151> 2000-12-08 <160> 25 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 4730 <212> DNA <213> Bos taurus <220> <221> CDS <222> (392)...(4597) <400> 1 cagtgttgag geggeaggat gtagagtget gtteaagett teeagtggag teecegaaaa 60 gggaaggcag agaaagacat cttctaaata acaaatagga ggagttacag tacctgactt 120 ggggctgctc ttaatcaagt gctgccgctg caaggaagat aattttcaag cgttatgaag 180 gcggagaagg attccgaaga cgaagaaaat atccttagag atccaagcta agtgtagtgc 240 agcatgaaga ttgcagaaca ggaagagttc taagaagaag gactgagtca ctagttagga 300 gtotototga gggotggott tgtgagocac agtgatttgt aacttaatgc gaactaattt 360 getqttaqea acaagaaact aaateetgte t atg atg age tgt tgg ttt tet Met Met Ser Cys Trp Phe Ser tgt gct cct aag aac aga caa gca gca gat tgg aac aaa tac gat gac Cys Ala Pro Lys Asn Arg Gln Ala Ala Asp Trp Asn Lys Tyr Asp Asp cqa ttg atg aga gca gaa agg gga gat gta gaa aaa gtg tcc tca Arg Leu Met Arg Ala Ala Glu Arg Gly Asp Val Glu Lys Val Ser Ser 30

45

60

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Ile Leu Ala Lys Lys Gly Val Asn Pro Gly Lys Leu Asp Val Glu Gly

aga tot god tit cat git gig god toa aag gga aat oit gag tigt tig

Arg Ser Ala Phe His Val Val Ala Ser Lys Gly Asn Leu Glu Cys Leu

aat gee ate etc ata cat gga gtt gat att aca ace agt gac ace gea

460

508

556

604

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cta Leu	caa Gln 105	aaa Lys	ctt Leu	cta Leu	cag Gln	tac Tyr 110	aat Asn	tgt Cys	ccc Pro	act Thr	gaa Glu 115	cat His	gta Val	gac Asp	ctg Leu	748
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aca Thr	ata Ile	tgt Cys 170	caa Gln	ctg Leu	ctg Leu	ata Ile	gat Asp 175	aga Arg	ggg Gly	gcg Ala	gat Asp	att Ile 180	aat Asn	tcc Ser	aga Arg	940
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ctg Leu	gac Asp	gcc Ala	ctt Leu	ggc Gly 220	cat His	gac Asp	agt Ser	tct Ser	tac Tyr 225	tat Tyr	gca Ala	aga Arg	att Ile	ggt Gly 230	gac Asp	1084
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ttg Leu	tct Ser 265	Gln	atg Met	cta Leu	gat Asp	gaa Glu 270	Val	aat Asn	acg Thr	aag Lys	tca Ser 275	Asn	cag Gln	agg Arg	gag Glu	1228
cat His 280	Gln	aac Asn	att Ile	cag Gln	gat Asp 285	Leu	gag Glu	att Ile	gaa Glu	aat Asn 290	Glu	gat Asp	ctg Leu	aaa Lys	gag Glu 295	1276
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_	_		_	_							_	ctg Leu		_	-	1468
	_				-	-						agt Ser				1516
	_		-							_		atg Met		_		1564
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									-		_	agg Arg				1804
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		_		_	_	_	ttg Leu				_	•			-	2284
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_		_			-	_	gaa Glu 655				-	_	_		_	2380
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	_	_			-		GJ Y G3G	_							_	2476
							gaa Glu									2524
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-				_	_	-	gaa Glu 735	_		_			_	~-		2620
		_				-	ctt Leu		-							2668
							aag Lys									2716
							gaa Glu									2764
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-	cag Gln	_		_					_	~ -	_	_				2860
	tat Tyr 825			_					_	_		_		_	_	2908
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	ata Ile															3100
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	cag Gln															3292
	gct Ala	_			_	_	_		-		_				~	3340
	gag Glu 985	Lys					Gln					Thr				3388
aat Asn 100	Thr		gaa Glu			ı Āl				s Ly		-		-	gac aag Asp Lys 101	5
tta Leu	aag Lys	aag Lys	gag Glu	atc Ile 1020	Lev	act 1 Thi	ctt Lei	caç ı Glr	g aag n Lys 102	s As	at ct sp Le	ca aa eu Ly	ag ga /s As	sp Ly	ag aat /s Asi )30	
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aca	gaa	gag	cto	g aac	aga	a cag	g tta	a aa	ıa ga	ıc ct	g tt	g ca	ig a	aa t	ac aca	a 3580

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ccg ctg gag ( Pro Leu Glu (	cag gtt ga Gln Val Gl 1100	g tcc ctg aaa 1 Ser Leu Lys	aaa tct ctt Lys Ser Leu 1105	agt ggt aca Ser Gly Thr 1110	atc 3724 Ile
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aac tcc tct Asn Ser Ser 1145	gtg ccc ct Val Pro Le	g gct gag ca u Ala Glu Hi 1150	at ttg cag gtt s Leu Gln Val 1155	Lys Glu Ala	ttt 3868 Phe
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Gln Asn Thr	aaa caa go Lys Gln Al 1195	g tta aaa aaa a Leu Lys Lys 120	a tta gag act s Leu Glu Thr 00	cgg gag gtg Arg Glu Val 1205	gtt 4012 Val
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gta tgt gag Val Cys Glu 1240 gat gag aag Asp Glu Lys	gag gtt ttg Glu Val Leu 124 gaa ttg ctc Glu Leu Leu 1260 cga tgt gac	123,0    cat gcc aaa His Ala Lys 5    cat ttc agc   His Phe Ser	Leu Asn Arg Line 1235  aag aag gaa ci Lys Lys Glu Li 1250  ata gag caa gi Ile Glu Gln Gi 1265  aca acc atc atc atc atc atc atc atc atc	ys Tyr Glu Gl  tg tct gct aa eu Ser Ala Ly 12 aa atc aaa ga lu Ile Lys As 1270 cg gag cta ca	u 4156 75 75 75 75 75 75 75 75 75 75 75 75 75

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170

175

Gly Ala Asp Ile Asn Ser Arg Asp Lys Gln Asn Arg Thr Ala Leu Met Leu Gly Cys Glu Tyr Gly Cys Lys Asp Ala Val Glu Val Leu Ile Lys Asn Gly Ala Asp Val Thr Leu Leu Asp Ala Leu Gly His Asp Ser Ser Tyr Tyr Ala Arg Ile Gly Asp Asn Leu Asp Ile Leu Thr Leu Leu Lys Thr Ala Ser Glu Asn Ser Asn Lys Gly Arg Glu Leu Trp Lys Lys Gly Pro Ser Leu Gln Gln Arg Asn Leu Ser Gln Met Leu Asp Glu Val Asn Thr Lys Ser Asn Gln Arg Glu His Gln Asn Ile Gln Asp Leu Glu Ile Glu Asn Glu Asp Leu Lys Glu Arg Leu Arg Lys Ile Gln Gln Gln Gln Arq Ile Leu Leu Asp Lys Val Asn Gly Leu Gln Leu Gln Leu Asn Glu Glu Val Met Val Ala Asp Asp Leu Glu Ser Glu Lys Glu Lys Leu Lys Ser Leu Leu Ala Ala Lys Glu Lys Gln His Glu Glu Ser Leu Arg Thr Ile Glu Ala Leu Lys Ser Arg Phe Lys Tyr Phe Glu Ser Asp His Leu Gly Ser Gly Ser His Phe Arg Lys Glu Asp Met Leu Leu Lys Gln Gly Gln Met Tyr Met Thr Asp Ser Gln Cys Thr Ser Thr Gly Met Pro Val His Met Gln Ser Arg Ser Met Leu Arg Pro Leu Glu Leu Ala Leu Pro Asn Gln Ala Ser Tyr Ser Glu Asn Glu Ile Leu Lys Lys Glu Leu Glu Ala Met Arg Thr Phe Cys Asp Ser Ala Lys Gln Asp Arg Leu Lys Leu Gln Asn Glu Leu Ala His Lys Val Ala Glu Cys Lys Ala Leu Ala Leu Glu Cys Glu Arg Val Lys Glu Asp Ser Asp Glu Gln Ile Lys Gln Leu Glu Asp Ala Leu Lys Asp Val Gln Lys Arg Met Tyr Glu Ser Glu Gly Lys Val Lys Gln Met Gln Thr His Phe Leu Ala Leu Lys Glu His Leu Thr Ser Asp Ala Ala Thr Gly Asn His Arg Leu Met Glu Glu Leu Lys Asp Gln Leu Lys Asp Met Lys Val Lys Tyr Glu Gly Ala Ser Ala Glu Val Gly Lys Leu Arg Asn Gln Ile Lys Gln Asn Glu Met Leu Val Glu Glu Phe Lys Arg Asp Glu Gly Lys Leu Met Glu Glu Asn Lys Arg Leu Gln Lys Glu Leu Ser Met Cys Glu Leu Glu Arg Glu Lys Arg Gly Arg Lys Leu Thr Glu Met Glu Gly Gln Leu Lys Asp Leu Ser Ala Lys Leu Ala Leu Ser Ile Pro Ala Glu Lys Phe Glu Asn Met Lys Ser Leu Leu Ser Asn Glu Leu Asn Glu Lys Ala Lys Lys Leu Ile Asp Val Glu Arg Glu Tyr Glu Arg Ser Leu Asn Glu Thr Arg Pro Leu Lys Arg Glu Leu Glu Asn Leu Lys Ala Lys Leu Ala Gln His Val Lys Pro Glu Glu His

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